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stDB - Fast Pairwise Comparison of Sequences
lease 5.4

sults file Seq140-aay87247.res made by tport on Wed 14 Jan 104 14:59:51 PST.

ery sequence being compared:US-10-006-485A-140 (1-311)
mber of sequences searched:                    1
mber of scores above cutoff:                   1

Results of the initial comparison of US-10-006-485A-140 (1-311) with:
     File : aay87247.pep
```
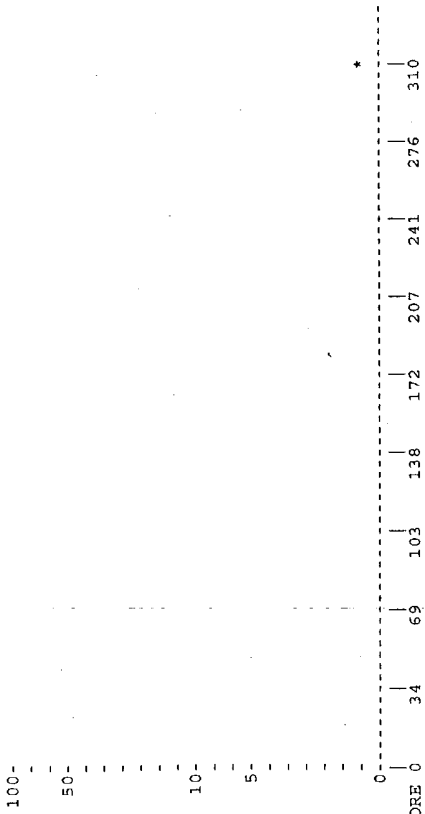
```
Sequence Name       Description                          Length  Init.  Opt.
                                                                 Score  Score   Sig.  Frame
------------------------------------------------------------------------------------------
 1. aay87247        Human signal peptide containi        311     310    310    0.00   0
```

```
1. US-10-006-485A-140 (1-311)
   aay87247      Human signal peptide containing protein HSPP-24 SE
```

```
Initial Score     =    310   Optimized Score =    310   Significance =   0.00
Residue Identity  =    99%   Matches         =    309   Mismatches   =      1
Gaps              =      0   Conservative Substitutions =    0
```

```
          X           10        20        30        40        50        60        70
MGVPTALEAGSWRWGSLLFALFLAASLGPVAAFKVATPYSLYVCPEGQNVTLTCRLLGPVDKGHDVTFYKTW
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
MGVPTAPEAGSWRWGSLLFALFLAASLGPVAAFKVATPYSLYVCPEGQNVTLTCRLLGPVDKGHDVTFYKTW
          X           10        20        30        40        50        60        70

               80        90       100       110       120       130       140
YRSSRGEVQTCSERRPIRNLTFQDLHLHHGHQAANTSHDLAQRHGLESASDHHGNFSITMRNLTLLDSGLY
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
YRSSRGEVQTCSERRPIRNLTFQDLHLHHGHQAANTSHDLAQRHGLESASDHHGNFSITMRNLTLLDSGLY
               80        90       100       110       120       130       140

             150       160       170       180       190       200       210
CCLVVEIRHHHSEHRVHGAMELQVQTGKDAPSNCVVYPSSSQDSENITAAALATGACIVGILCLPLILLLVY
||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||
CCLVVEIRHHHSEHRVHGAMELQVQTGKDAPSNCVVYPSSSQESENITAAALATGACIVGILCLPLILLLVY
             150       160       170       180       190       200       210

          220       230       240       250       260       270       280
KQRQAASNRRAQELVRMDSNIQGIENPGFEASPPAQGIPEAKVRHPLSYVAQRQPSESGRHLLSEPSTPLSP
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
KQRQAASNRRAQELVRMDSNIQGIENPGFEASPPAQGIPEAKVRHPLSYVAQRQPSESGRHLLSEPSTPLSP
          220       230       240       250       260       270       280

    290       300       X
PGPGDVFFPSLDPVPDSPNFEVI
|||||||||||||||||||||||
PGPGDVFFPSLDPVPDSPNFEVI
    290       300       310
```

```
       PARAMETERS

milarity matrix      PAM-150   K-tuple              1
reshold level of sim.   16%
smatch penalty         1       Joining penalty     20
p penalty            5.00      Window size        311
p size penalty       0.05
toff score             1
ndomization group      0

       SEARCH STATISTICS

               Mean     Median     Standard Deviation
               310        0              0.00

      CPU                     Total Elapsed
00:00:00.00                   00:00:00.00

mber of residues:           311
mber of sequences searched:   1
mber of scores above cutoff:  1

he scores below are sorted by initial score.
ignificance is calculated based on initial score.

100% identical sequence to the query sequence was not found.

he list of best scores is:
```

```
ORE  0    34    69   103   138   172   207   241   276   310
DEV                                                      *
```